Please replace the paragraph beginning at line 19 of page 12 with the following rewritten paragraph:

--Figure 1 (A, B) depicts a schematic representation of the various vectors, reagents and process steps used in the construction of the chimeric DNA molecule encoding a chimeric protein in which is conserved the structure of the natural form of sIL-6R ending at the Val 356 residue followed by the sequence of the natural, mature, processed form of IL-6, as detailed in Example 1. In Fig. 1A, the reverse primer is complementary to SEQ ID NO:9 and in Fig. 1B, the EcoRI enzyme recognition site and the strand of the IL-6 cDNA sequence is presented as SEQ ID NO:10.--

C2

Please replace the paragraph beginning at line 7 of page 13 with the following rewritten paragraph:

--Figure 3 depicts the amino acid sequence (one-letter code) (SEQ ID NO:7) of the sIL-6RδVal/IL-6 chimera in which is shown the different domains of the molecule, including the N-terminal signal peptide (line on top of sequence), the immunoglobulin-like (Ig-like) domain, the cytokine receptor N-domain (underlined), the cytokine C-domain (line on top of sequence) and the receptor pre-membrane region (the region between the C-domain and the transmembranal domain), all of the sIL-6R part of the chimera; as well as the mature IL-6 moiety (underlined below) of the chimera, as described in Examples 1 and 2;--

C3

Please replace the paragraph beginning at line 1 of page 15 with the following rewritten paragraph:

C4

--Figure 11 depicts the amino acid sequence (one letter code) (SEQ ID NO:8) of the IL-6-sIL-6RδVal chimera 3e, the linker being underlined; and--

Please replace the paragraph beginning at line 10 of page 30 with the following rewritten paragraph:

C5

--As indicated above, an advantageous characteristic of the sIL-6RδVal/IL-6 construct is that it is essentially the fusion of the natural form of sIL-6R and of the natural form of IL-6 as they exist in the human body, and without extraneous polypeptide sequences. However, the conservation of the EcoRI site in the sIL-6RδVal/IL-6 construct (Figure 1) allows to easily introduce linker polypeptide segments between the sIL-6R and the IL-6 moieties. One such construct with the 13-amino acid linker sequence Glu-Phe-Gly-Ala-Gly-Leu-Val-Leu-Gly-Gly-Gln-Phe-Met (SEQ ID NO:1) introduced between Val-356 of sIL-6R and Pro-29 of IL-6, was also constructed (sIL-6RδVal/L/IL-6).--

Please replace the paragraph beginning at line 1 of page 41 with the following rewritten paragraph:

C6

-- SpeI SmaI BamH1

5' CT AGT GGG CCC GGG GTG GCG GG (SEQ ID NO:2)

A CCC GGG CCC CAC CGC CCC TAG 5' (SEQ ID NO:12)--

Please replace the paragraph beginning at line 19 of page 41 with the following rewritten paragraph:

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SmaI

5' GAT CCG GGC GGC GGG GGA GGG GGG CCC GGG C[NcoI] (SEQ ID NO:5)

[BamH1] GC CCG CCG CCC CCT CCT CCC GGG CCC GGT AC 5'

(SEQ ID NO:11)--

IN THE CLAIMS

Please amend claims 5 and 7 as follows:

5 (Amended). A chimeric sIL-6R/IL-6 protein and biologically active analogs thereof according to claim 2, wherein said linker is a peptide of 13 amino acid residues of sequence E-F-G-A-G-L-V-L-G-G-Q-F-M (Glu-Phe-Gly-Ala-Gly-Leu-Val-Leu-Gly-Gly-Gln-Phe-Met) (SEQ ID NO:1).

7 (Amended). A chimeric sIL-6R/IL-6 protein according to claim 1, being the herein designated sIL-6RδVal/L/IL-6 having a 13 amino acid peptide linker of sequence E-F-G-A-G-L-V-L-G-G-Q-F-M (SEQ ID NO:1) between the C-terminal Val-356 of sIL-6R and the N-terminal Pro-29 of IL-6, said chimeric protein having the sequence set forth in Fig. 3 wherein the tripeptide of sequence E-F-M between positions 357-359 of Fig. 3 is replaced by said 13 amino acid peptide sequence.

IN THE SEQUENCE LISTING

Please substitute the attached Sequence Listing (numbered as pages 1-8) for the one previously submitted as pages 47-53 and renumber the subsequent pages accordingly.